WHAT IS CLAIMED IS:

1. A method for associating a gene **G** in the genome of a first species with a clinical trait **T** exhibited by said first species and a second species, the method comprising:

(a) identifying an expression quantitative trait loci (eQTL) for a gene **G′** in said second species that is an ortholog of said gene **G** using a first quantitative trait loci (QTL) analysis, wherein said first QTL analysis uses a plurality of expression statistics for said gene **G′** as a quantitative trait, wherein each expression statistic in said plurality of expression statistics represents an expression value for said gene **G′** in an organism in a plurality of organisms of said second species;

(b) identifying a clinical quantitative trait loci (cQTL) that is linked to said clinical trait **T** using a second QTL analysis, wherein said second QTL analysis uses a plurality of phenotypic values as a quantitative trait, wherein each phenotypic value in said plurality of phenotypic values represents a phenotypic value for said clinical trait **T** in an organism in said plurality of organisms of said second species; and

(c) determining whether said eQTL and said cQTL colocalize to the same locus in the genome of said second species, wherein, when said eQTL and said cQTL colocalize to the same locus, said gene **G** is associated with said clinical trait **T** in said first species.

2. The method of claim 1, wherein said determining step (c) further comprises determining whether the locus of said eQTL in the genome of said second species corresponds to the physical location of said gene **G′** in the genome of said second species, wherein, when said locus of said eQTL in the genome of said second species corresponds to the physical location of said gene **G′** in the genome of said second species said gene **G** is associated with said clinical trait **T**.

3. The method of claim 2, wherein said eQTL corresponds to the physical location of said gene **G′** when the eQTL and said gene **G′** colocalize within 3cM of each other in the genome of said second species.

4. The method of claim 2, wherein said eQTL corresponds to the physical location of said gene **G′** when the eQTL and said gene **G′** colocalize within 1cM of each other in the genome of said second species.

5. The method of claim 1, the method further comprising testing whether a colocalization of said eQTL and said cQTL is caused by pleiotropy.

6. The method of claim 1, wherein said first QTL analysis and said second QTL analysis each uses a genetic marker map that represents the genome of said second species.

7. The method of claim 6, which further comprises, prior to said identifying step (a), a step of constructing said genetic marker map from a set of genetic markers associated with a plurality of organisms representing said second species.

8. The method of claim 7, wherein said set of genetic markers comprises single nucleotide polymorphisms (SNPs), microsatellite markers, restriction fragment length polymorphisms, short tandem repeats, DNA methylation markers, sequence length polymorphisms, random amplified polymorphic DNA, amplified fragment length polymorphisms, or simple sequence repeats.

9. The method of claim 7, wherein genotype data is used in said constructing step and wherein said genotype data comprises knowledge of which alleles, for each marker in said set of genetic markers, are present in each organism in said plurality of organisms representing said second species.

10. The method of claim 7, wherein said plurality of organisms representing said second species represents a segregating population and pedigree data is used in said constructing step, and wherein said pedigree data shows one or more relationships between organisms in said plurality of organisms representing said second species.

11. The method of claim 10, wherein said plurality of organisms representing said second species comprises an F2 population, a F_t population, a $F_{2:3}$ population, or a Design III population and said one or more relationships between organisms in said plurality of organisms representing said second species indicates which organisms in said plurality of organisms representing said second species are members of said F2 population, said F_t population, said $F_{2:3}$ population, or said Design III population.

12. The method of claim 1, wherein each said expression value is a normalized expression level measurement for said gene **G′** in an organism in said plurality of organisms of said second species.

13. The method of claim 12, wherein each said expression level measurement is determined by measuring an amount of a cellular constituent encoded by said gene **G′** in one or more cells from an organism in said plurality of organisms of said second species.

14. The method of claim 13, wherein said amount of said cellular constituent comprises an abundance of an RNA present in said one or more cells of said organism.

15. The method of claim 14, wherein said abundance of said RNA is measured by a method comprising contacting a gene transcript array with said RNA from said one or more cells of said organism, or with nucleic acid derived from said RNA, wherein said gene transcript array comprises a positionally addressable surface with attached nucleic acids or nucleic acid mimics, wherein said nucleic acids or nucleic acid mimics are capable of hybridizing with said RNA species, or with nucleic acid derived from said RNA species.

16. The method of claim 12, wherein said normalized expression level measurement is obtained by a normalization technique selected from the group consisting of Z-score of intensity, median intensity, log median intensity, Z-score standard deviation log of intensity, Z-score mean absolute deviation of log intensity, calibration DNA gene set, user normalization gene set, ratio median intensity correction, and intensity background correction.

17. The method of claim 1, wherein said first QTL analysis comprises:

(i) testing for linkage between (a) the genotype of said plurality of organisms of said second species at a position in the genome of said second species and (b) said plurality of expression statistics for said gene **G′**;

(ii) advancing the position in said genome by an amount; and

(iii) repeating steps (i) and (ii) until all or a portion of the genome of said second species has been tested.

18. The method of claim 17, wherein said amount is less than 100 centiMorgans.

19. The method of claim 17, wherein said amount is less than 10 centiMorgans.

20. The method of claim 17, wherein said amount is less than 5 centiMorgans.

21. The method of claim 17, wherein said amount is less than 2.5 centiMorgans.

22. The method of claim 17, wherein said testing comprises performing linkage analysis or association analysis.

23. The method of claim 22, wherein said linkage analysis or association analysis generates a statistical score for said position in the genome of said second species.

24. The method of claim 23, wherein said testing is linkage analysis and said statistical score is a logarithm of the odds (lod) score.

25. The method of claim 24, wherein said eQTL is represented by a lod score that is greater than 2.0.

26. The method of claim 24, wherein said eQTL is represented by a lod score that is greater than 3.0.

27. The method of claim 24, wherein said eQTL is represented by a lod score that is greater than 4.0.

28. The method of claim 24, wherein said eQTL is represented by a lod score that is greater than 5.0.

29. The method of claim 1, wherein said second QTL analysis comprises:

(i) testing for linkage between (a) the genotype of said plurality of organisms of said second species at a position in the genome of said second species and (b) said plurality of phenotypic values;

(ii) advancing the position in said genome by an amount; and

(iii) repeating steps (i) and (ii) until all or a portion of the genome of said second species has been tested.

30. The method of claim 29, wherein said amount is less than 100 centiMorgans.

31. The method of claim 29, wherein said amount is less than 10 centiMorgans.

32. The method of claim 29, wherein said amount is less than 5 centiMorgans.

33. The method of claim 29, wherein said amount is less than 2.5 centiMorgans.

34. The method of claim 29, wherein said testing comprises performing linkage analysis or association analysis.

35. The method of claim 34, wherein said linkage analysis or association analysis generates a statistical score for said position in the genome of said second species.

36. The method of claim 35, wherein said testing is linkage analysis and said statistical score is a logarithm of the odds (lod) score.

37. The method of claim 36, wherein said cQTL is represented by a lod score that is greater than 2.0.

38. The method of claim 36, wherein said cQTL is represented by a lod score that is greater than 3.0.

39. The method of claim 36, wherein said cQTL is represented by a lod score that is greater than 4.0.

40. The method of claim 36, wherein said cQTL is represented by a lod score that is greater than 5.0.

41. The method of claim 1, wherein said first species is human.

42. The method of claim 1, wherein said second species is a plant or an animal.

43. The method of claim 1, wherein said second species is corn, beans, rice, tobacco, potatoes, tomatoes, cucumbers, apple trees, orange trees, cabbage, lettuce, or wheat.

44. The method of claim 1, wherein said second species is a mammal, a primate, mice, rats, dogs, cats, chickens, horses, cows, pigs, or monkeys.

45. The method of claim 1, wherein said second species is Drosophila, yeast, a virus, or Caenorhabditis elegans.

46. The method of claim 1, wherein said clinical trait **T** is a complex trait.

47. The method of claim 46, wherein said complex trait **T** is characterized by an allele that exhibits incomplete penetrance in said second species.

48. The method of claim 46, wherein said complex trait is a disease that is contracted by an organism in said plurality of organisms of said second species, and wherein said organism inherits no predisposing allele to said disease.

49. The method of claim 46, wherein said complex trait arises when any of a plurality of different genes in the genome of said second species is somatically mutated.

50. The method of claim 46, wherein said complex trait requires the simultaneous presence of mutations in a plurality of genes in the genome of said second species.

51. The method of claim 46, wherein said complex trait is associated with a high frequency of disease-causing alleles in said second species.

52. The method of claim 46, wherein said complex trait is a phenotype that does not exhibit Mendelian recessive or dominant inheritance attributable to a single gene locus.

53. The method of claim 46, wherein said complex trait is asthma, ataxia telangiectasia, bipolar disorder, cancer, common late-onset Alzheimer's disease, diabetes, heart disease, hereditary early-onset Alzheimer's disease, hereditary nonpolyposis colon cancer, hypertension, infection, maturity-onset diabetes of the young, mellitus, migraine, nonalcoholic fatty liver, nonalcoholic steatohepatitis, non-insulin-dependent diabetes mellitus, obesity, polycystic kidney disease, psoriases, schizophrenia, or xeroderma pigmentosum.

54. The method of claim 1, wherein said eQTL and said cQTL colocalize to the same locus in the genome of said second species when the physical location of the eQTL in said genome is within 40 cM of the physical location of the cQTL in said genome.

55. The method of claim 1, wherein said eQTL and said cQTL colocalize to the same locus in the genome of said second species when the physical location of the eQTL in said genome is within 20 cM of the physical location of the cQTL in said genome.

56. The method of claim 1, wherein said eQTL and said cQTL colocalize to the same locus in the genome of said second species when the physical location of the eQTL in said genome is within 10 cM of the physical location of the cQTL in said genome.

57. The method of claim 1, wherein said eQTL and said cQTL colocalize to the same locus in the genome of said second species when the physical location of the eQTL in said genome is within 6 cM of the physical location of the cQTL in said genome.

58. A computer program product for use in conjunction with a computer system, the computer program product comprising a computer readable storage medium and a computer program mechanism embedded therein, the computer program mechanism for associating a gene **G** in the genome of a first species with a clinical trait **T** exhibited by said first species and a second species, the computer program mechanism comprising:

an expression quantitative trait loci (eQTL) identification module for identifying an expression quantitative trait loci (eQTL) for a gene **G′** in said second species that is an ortholog of said gene **G** using a first quantitative trait loci (QTL) analysis, wherein said first QTL analysis uses a plurality of expression statistics for said gene **G′** as a quantitative trait, wherein each expression statistic in said plurality of expression statistics represents an expression value for said gene **G′** in an organism in said plurality of organisms of said second species;

a clinical quantitative trait loci (cQTL) identification module for identifying a clinical quantitative trait loci (cQTL) that is linked to said clinical trait **T** using a second QTL analysis, wherein said second QTL analysis uses a plurality of phenotypic values as a quantitative trait, wherein each phenotypic value in said plurality of phenotypic values represents a phenotypic value for said clinical trait **T** in an organism in said plurality of organisms of said second species; and

a determination module for determining whether said eQTL and said cQTL colocalize to the same locus in the genome of said second species, wherein, when said eQTL and said cQTL colocalize to the same locus, said gene **G** is associated with said clinical trait **T** in said first species.

59. A computer system for associating a gene **G** in the genome of a first species with a clinical trait **T** exhibited by said first species and a second species, the computer system comprising:

a central processing unit;

a memory coupled to the central processing unit, the memory storing an expression quantitative trait loci (eQTL) identification module, a clinical quantitative trait loci (cQTL) identification module, and a determination module; wherein

the expression quantitative trait loci (eQTL) identification module comprises instructions for identifying an expression quantitative trait loci (eQTL) for a gene **G′** in said second species that is an ortholog of said gene **G** using a first quantitative trait loci (QTL) analysis, wherein said first QTL analysis uses a plurality of expression statistics for gene **G′** as a quantitative trait, wherein each expression statistic in said plurality of expression statistics represents an expression value for said gene **G′** in an organism in a plurality of organisms of said second species;

the clinical quantitative trait loci (cQTL) identification module comprises instructions for identifying a clinical quantitative trait loci (cQTL) that is linked to said clinical trait **T** using a second QTL analysis, wherein said second QTL analysis uses a plurality of phenotypic values as a quantitative trait, wherein each phenotypic value in said plurality of phenotypic values represents a phenotypic value for said clinical trait **T** in an organism in said plurality of organisms of said second species; and

the determination module comprises instructions for determining whether said eQTL and said cQTL colocalize to the same locus in the genome of said second species, wherein, when said eQTL and said cQTL colocalize to the same locus, said gene **G** is associated with said clinical trait **T**.

60. A method for associating a gene **G** in the genome of a first species with a clinical trait **T** exhibited by said first species and a second species, the method comprising:

(a) clustering quantitative trait locus data from a plurality of quantitative trait locus analyses to form a quantitative trait locus interaction map, wherein

each quantitative trait locus analysis in said plurality of quantitative trait locus analyses is performed for a gene in a plurality of genes in the genome of said second species using a genetic marker map and a quantitative trait in order to produce said quantitative trait locus data, wherein, for each quantitative trait locus analysis, said quantitative trait comprises an expression statistic for the gene for which the quantitative trait locus analysis is performed, for each organism in a plurality of organisms of said second species; and wherein

said genetic marker map is constructed from a set of genetic markers associated with said plurality of organisms of said second species; and

(b) analyzing said quantitative trait locus interaction map to identify a gene **G'** of said second species that is associated with said clinical trait **T**, wherein said gene **G'** is an ortholog of said gene **G** in said first species, thereby associating a gene **G** in the genome of said first species with said clinical trait **T**.

61. The method of claim 60, which further comprises, prior to said clustering step, a step of performing each said quantitative trait locus analysis in said plurality of quantitative trait locus analyses.

62. The method of claim 60, wherein said expression statistic for said gene **G'** is computed by a method comprising transforming an expression level measurement of said gene **G'** from each organism in said plurality of organisms of said second species.

63. The method of claim 60, wherein each said quantitative trait locus analysis comprises:

(i) testing for linkage between a position in a chromosome, in the genome of said second species, and the quantitative trait used in the quantitative trait locus analysis;

(ii) advancing the position in said chromosome by an amount; and

(iii) repeating steps (i) and (ii) until all or a portion of the genome has been tested.

64. The method of claim 63, wherein said quantitative trait locus data produced from each respective quantitative trait locus analysis comprises a logarithmic of the odds score computed at each said position.

65. The method of claim 63, wherein said testing comprises performing linkage analysis or association analysis.

66. The method of claim 60, wherein said clustering of the quantitative trait locus data from each said quantitative trait locus analysis comprises applying a hierarchical clustering technique, applying a k-means technique, applying a fuzzy k-means technique, applying a Jarvis-Patrick clustering, applying a self-organizing map technique, or applying a neural network technique.

67. The method of claim 62, which further comprises constructing a gene expression cluster map from each expression statistic created by said transforming step.

68. The method of claim 67, wherein said constructing a gene expression cluster map comprises:

creating a plurality of gene expression vectors, each gene expression vector in said plurality of gene expression vectors representing an expression level measurement of a gene, in said plurality of genes in the genome of said second species, in each of the plurality of organisms of said second species;

computing a plurality of correlation coefficients, wherein each correlation coefficient in said plurality of correlation coefficients is computed between a gene expression vector pair in said plurality of gene expression vectors; and

clustering said plurality of gene expression vectors based on said plurality of correlation coefficients in order to form said gene expression cluster map.

69. The method of claim 68, wherein said step of analyzing said quantitative trait locus interaction map comprises filtering the quantitative trait locus interaction map in order to obtain a candidate pathway group; wherein the filtering comprises identifying a quantitative trait locus in said candidate pathway group in said gene expression cluster map.

70. The method of claim 67, wherein said constructing a gene expression cluster map comprises:

creating a plurality of gene expression vectors, each gene expression vector in said plurality of gene expression vectors representing a gene in said plurality of genes;

computing a plurality of metrics, wherein each metric in said plurality of metrics is computed between a gene expression vector pair in said plurality of gene expression vectors; and

clustering said plurality of gene expression vectors based on said plurality of metrics in order to form said gene expression cluster map.

71. The method of claim 60, wherein said plurality of genes comprises at least five genes.

72. A computer program product for use in conjunction with a computer system, the computer program product comprising a computer readable storage medium and a computer program mechanism embedded therein, the computer program mechanism comprising:

a clustering module for clustering quantitative trait locus data from a plurality of quantitative trait locus analyses to form a quantitative trait locus interaction map; wherein

each quantitative trait locus analysis in said plurality of quantitative trait locus analyses is performed for a gene in a plurality of genes in the genome of a second species using a genetic marker map and a quantitative trait in order to produce said quantitative trait locus data, wherein, for each quantitative trait locus analysis, said quantitative trait comprises an expression statistic for the gene for which the quantitative trait locus analysis is performed, for each organism in a plurality of organisms of said second species; and wherein

said genetic marker map is constructed from a set of genetic markers associated with said plurality of organisms of said second species;

an analysis module for analyzing said quantitative trait locus interaction map to identify a gene **G′** in said second species that is associated with a clinical trait **T** exhibited by a first species and said second species, wherein said gene **G′** is an ortholog of a gene **G** in said first species.

73. A computer system for associating a gene **G** in the genome of a first species with a clinical trait **T** exhibited by said first species and a second species, the computer system comprising:

a central processing unit;

a memory, coupled to the central processing unit, the memory storing a clustering module, an analysis module and an ortholog identification module;

the clustering module for clustering quantitative trait locus data from a plurality of quantitative trait locus analyses to form a quantitative trait locus interaction map; wherein

each quantitative trait locus analysis in said plurality of quantitative trait locus analyses is performed for a gene in a plurality of genes in the genome of said second species using a genetic marker map and a quantitative trait in order to produce said quantitative trait locus data, wherein, for each quantitative trait locus analysis, said quantitative trait comprises an expression statistic for the gene for which the quantitative

trait locus analysis is performed, for each organism in a plurality of organisms of said second species; and wherein

said genetic marker map is constructed from a set of genetic markers associated with said plurality of organisms of said second species;

the analysis module for analyzing said quantitative trait locus interaction map to identify a gene **G′** of said second species that is associated with a clinical trait **T** exhibited by said first species and said second species, wherein said gene **G′** is an ortholog of said gene **G** of said first species.

74. A method for identifying a quantitative trait locus for a complex trait in a first species, wherein the complex trait is exhibited by said first species and a second species, the method comprising:

(a) dividing a plurality of organisms of said second species into a plurality of subpopulations using a classification scheme that classifies each organism in said plurality of organisms of said second species into at least one of said subpopulations, wherein said classification scheme uses a plurality of cellular constituent measurements from each said organism of said second species; and

(b) for at least one subpopulation in said plurality of subpopulations, performing quantitative genetic analysis on said subpopulation in order to identify a quantitative trait locus for said complex trait in said second species, wherein said quantitative trait locus for said complex trait in said second species is an ortholog of the quantitative trait loci in said first species, thereby identifying said quantitative trait locus for said complex trait in said first species.

75. The method of claim 74, wherein said complex trait is a disease that is contracted by an organism in said first species or said second species, and wherein said organism inherits no predisposing allele to said disease.

76. The method of claim 74, wherein said complex trait arises when any of a plurality of different genes in the genome of said first species or said second species is mutated.

77. The method of claim 74, wherein said complex trait is associated with a high frequency of disease-causing alleles in said first species or said second species.

78. The method of claim 74, wherein said complex trait is a phenotype that does not exhibit Mendelian recessive or dominant inheritance attributable to a gene locus.

79. The method of claim 74, wherein said complex trait is asthma, ataxia telangiectasia, bipolar disorder, cancer, common late-onset Alzheimer's disease, diabetes, heart disease, hereditary early-onset Alzheimer's disease, hereditary nonpolyposis colon cancer, hypertension, infection, maturity-onset diabetes of the young, mellitus, migraine, nonalcoholic fatty liver, nonalcoholic steatohepatitis, non-insulin-dependent diabetes mellitus, obesity, polycystic kidney disease, psoriases, schizophrenia, or xeroderma pigmentosum.

80. The method of claim 74, wherein said plurality of cellular constituent measurements from each said organism of said second species comprises the measurement of the cellular constituent levels of ten or more cellular constituents in each said organism.

81. The method of claim 74, wherein said dividing comprises determining whether a class predictor is available, and

when a class predictor is available, using a supervised classification scheme to classify each organism in said plurality of organisms of said second species into a subpopulation in said plurality of subpopulations; and

when a class predictor is not available, using an unsupervised classification scheme to classify each organism in said plurality of organisms of said second species into a subpopulation in said plurality of subpopulations.

82. The method of claim 74, wherein said classification scheme is a supervised classification scheme.

83. The method of claim 74, wherein said classification scheme is an unsupervised classification scheme.

84. The method of claim 83, wherein said unsupervised classification scheme is a hierarchical cluster analysis that uses a nearest-neighbor algorithm, a farthest-

neighbor algorithm, an average linkage algorithm, a centroid algorithm, or a sum-of-squares algorithm to determine the similarity between (i) the plurality of cellular constituent measurements from one organism in said plurality of organisms of said second species and (ii) the plurality of cellular constituent measurements from another organism in said plurality of organisms of said second species.

85. A computer program product for use in conjunction with a computer system, the computer program product comprising a computer readable storage medium and a computer program mechanism embedded therein, the computer program mechanism comprising:

a classification module for dividing a plurality of organisms of a second species into a plurality of subpopulations using a classification scheme that classifies each organism in said plurality of organisms of said second species into at least one of said subpopulations, wherein said classification scheme uses a plurality of cellular constituent measurements from each said organism in said second species;

a genetic analysis module that, for at least one subpopulation in said plurality of subpopulations, performs quantitative genetic analysis on said subpopulation in order to identify a quantitative trait locus for a complex trait that is exhibited by said second species and a first species, wherein said quantitative trait locus for said complex trait that is exhibited by said second species is the ortholog of the quantititative trait locus of said first species.

86. A computer system for identifying a quantitative trait locus for a complex trait in a first species, wherein the complex trait is exhibited by said first species and a second species, the computer system comprising:

a central processing unit;

a memory, coupled to the central processing unit, the memory storing a classification module, and a genetic analysis module; wherein

the classification module includes instructions for dividing a plurality of organisms of a second species into a plurality of subpopulations using a classification scheme that classifies each organism in said plurality of organisms of said second species into at least one of said subpopulations, wherein said classification scheme uses a plurality of cellular constituent measurements from each said organism in said second species;

the genetic analysis module includes instructions that, for at least one subpopulation in said plurality of subpopulations, performs quantitative genetic analysis on said subpopulation in order to identify said quantitative trait locus in said second species for said complex trait, wherein the quantitative trait locus in said second species is the ortholog of the quantitative trait locus in said first species.

87. A method for determining whether a candidate molecule affects a body weight disorder associated with an organism, comprising:

(a) contacting a cell from said organism with, or recombinantly expressing within the cell from said organism, said candidate molecule;

(b) determining whether the RNA expression or protein expression in said cell of at least one open reading frame is changed in step (a) relative to the expression of said open reading frame in the absence the candidate molecule, each said open reading frame being regulated by a promoter native to a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 9, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 16, SEQ ID NO: 19, SEQ ID NO: 20, and homologs of each of the foregoing; and

(c) determining that the candidate molecule affects a body weight disorder associated with said organism when the RNA expression or protein expression of said at least one open reading frame is changed, or

determining that the candidate molecule does not affect a body weight disorder associated with said organism when the RNA expression or protein expression of said at least one open reading frame is unchanged.

88. The method of claim 87 wherein a cell from said organism contacted with the candidate molecule exhibits a lower expression level of a protein sequence selected from the group consisting of SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, and SEQ ID NO: 29 than a cell from said organism that is not contacted with said candidate molecule.

89. The method of claim 87, wherein step (b) comprises determining whether RNA expression is changed.

90. The method of claim 87, wherein step (b) comprises determining whether protein expression is changed.

91. The method of claim 87, wherein step (b) comprises determining whether RNA or protein expression of at least two of said open reading frames is changed.

92. The method of claim 87, wherein step (a) comprises contacting the cell with the candidate molecule, and wherein step (a) is carried out in a liquid high throughput-like assay.

93. The method of claim 87, wherein the cell comprises a promoter region of at least one gene selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 9, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 16, SEQ ID NO: 19, SEQ ID NO: 20, and homologs of each of the foregoing, each promoter region being operably linked to a marker gene; and wherein step (b) comprises determining whether the RNA expression or protein expression of the marker gene(s) is changed in step (a) relative to the expression of said marker gene in the absence of the candidate molecule.

94. The method of claim 93, wherein the marker gene is selected from the group consisting of green fluorescent protein, red fluorescent protein, blue fluorescent protein, luciferase, LEU2, LYS2, ADE2, TRP1, CAN1, CYH2, GUS, CUP1 and chloramphenicol acetyl transferase.

95. The method of claim 87, wherein said body weight disorder is obesity, anorexia nervosa, bulimia nervosa or cachexia.

96. A method of identifying a molecule that specifically binds to a ligand selected from the group consisting of (i) a protein encoded by a gene selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 9, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 16, SEQ ID NO: 19, SEQ ID NO: 20, and

homologs of each of the foregoing, and (ii) a biologically active fragment of SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, and SEQ ID NO: 29, the method comprising:

(a) contacting the ligand with one or more candidate molecules under conditions conducive to binding between the ligand and the candidate molecules; and

(b) identifying a molecule within the one or more candidate molecules that binds to the ligand.

97. A purified protein comprising the amino acid sequence of SEQ ID NO: 8.

98. A purified protein encoded by a nucleic acid hybridizable under conditions of high stringency to a DNA having a sequence consisting of the coding region of SEQ ID NO: 2.

99. A purified protein comprising an amino acid sequence that has at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 8, in which percentage identity is determined over an amino acid sequence of identical size as SEQ ID NO: 8.

100. A purified protein comprising an amino acid sequence that has at least 95% identity to the amino acid sequence set forth in SEQ ID NO: 8, in which percentage identity is determined over an amino acid sequence of identical size as SEQ ID NO: 8.

101. An isolated nucleic acid comprising the nucleotide sequence of SEQ ID NO: 2, a coding region of SEQ ID NO: 2, SEQ ID NO: 3, a coding region of SEQ ID NO: 3, or the complement of any of the foregoing.

102. The isolated nucleic acid of claim 101 that is a DNA.

103. An isolated nucleic acid comprising a nucleotide sequence encoding the protein of any one of claims 97-100, or the complement thereof.

104. A recombinant cell containing the nucleic acid of claim 101, in which the nucleotide sequence is under the control of a promoter heterologous to the nucleotide sequence.

105. A recombinant cell containing a nucleic acid vector that comprises the nucleic acid of claim 101.

106. An antibody that binds to a protein consisting of the amino acid sequence of SEQ ID NO: 8.

107. The antibody of claim 106 that is monoclonal.

108. A molecule comprising a fragment of the antibody of claim 106, which fragment binds a protein consisting of the amino acid sequence of SEQ ID NO: 8.

109. A method of producing protein comprising:

growing a recombinant cell containing the nucleic acid of any one of claims 101-103 in which said nucleic acid sequence is under the control of a promoter heterologous to said nucleotide sequence, such that the protein encoded by said nucleic acid is expressed by the cell; and

recovering the expressed protein.

110. An isolated protein that is the product of the process of claim 109.

111. A pharmaceutical composition comprising a therapeutically effective amount of the protein of any one of claims 97-103, and a pharmaceutically acceptable carrier.

112. A pharmaceutical composition comprising a therapeutically effective amount of the nucleic acid of any one of claims 101-103; and a pharmaceutically acceptable carrier.

113. A pharmaceutical composition comprising a therapeutically effective amount of the recombinant cell of claim 104 or claim 105; and a pharmaceutically acceptable carrier.

114. A pharmaceutical composition comprising a therapeutically effective amount of an antibody that binds to a protein comprising the amino acid sequence of any one of claims 97-100, and a pharmaceutically acceptable carrier.

115. A method of treating or preventing a body weight disorder comprising administering to a subject in which treatment is desired a therapeutically effective amount of a molecule that antagonizes in the subject a protein comprising SEQ ID NO: 8, SEQ ID NO: 11, SEQ ID NO: 15, SEQ ID NO: 18, SEQ ID NO: 25, SEQ ID NO: 26, or SEQ ID NO: 27.

116. The method of claim 115 wherein said subject is human.

117. The method of claim 115 in which the molecule that inhibits a function of one or more of the group consisting of SEQ ID NO: 8, SEQ ID NO: 11, SEQ ID NO: 15, SEQ ID NO: 18, SEQ ID NO: 25, SEQ ID NO: 26, and SEQ ID NO: 27 is selected from the group consisting of an antibody that binds to one of SEQ ID NO: 8, SEQ ID NO: 11, SEQ ID NO: 15, SEQ ID NO: 18, SEQ ID NO: 25, SEQ ID NO: 26, and SEQ ID NO: 27 or a fragment or derivative therefore containing the binding region thereof, a nucleic acid complementary to the RNA produced by transcription of a gene encoding one of SEQ ID NO: 8, SEQ ID NO: 11, SEQ ID NO: 15, SEQ ID NO: 18, SEQ ID NO: 25, SEQ ID NO: 26, and SEQ ID NO: 27.

118. The method of claim 115 in which the molecule that inhibits a function of one or more of the group consisting of SEQ ID NO: 8, SEQ ID NO: 11, SEQ ID NO: 15, SEQ ID NO: 18, SEQ ID NO: 25, SEQ ID NO: 26, and SEQ ID NO: 27 is an oligonucleotide that

(a) consists of at least six nucleotides;

(b) comprises a sequence complementary to at least a portion of an RNA transcript of a gene encoding one of SEQ ID NO: 8, SEQ ID NO: 11, SEQ ID NO: 15, SEQ ID NO: 18, SEQ ID NO: 25, SEQ ID NO: 26 or SEQ ID NO: 27; and

(c) is hybridizable to said RNA transcript under moderately stringent conditions.

119. A method of treating or preventing a body weight disorder comprising administering to a subject in which treatment is desired a therapeutically effective amount of a molecule that enhances a function of one or more of the group consisting of SEQ ID NO: 8, SEQ ID NO: 11, SEQ ID NO: 15, SEQ ID NO: 18, SEQ ID NO: 25, SEQ ID NO: 26, and SEQ ID NO: 27.

120. The method of claim 119 wherein said subject is human.

121. A method of diagnosing a disease or disorder or the predisposition to said disease or disorder, wherein the disease or disorder is characterized by an aberrant level of one of SEQ ID NO: 1 through SEQ ID NO: 29 in a subject, the method comprising measuring the level of any one of SEQ ID NO: 1 through SEQ ID NO: 29 in a sample derived from the subject, in which an increase or decrease in the level of one of SEQ ID NO: 1 through SEQ ID NO: 29 in said sample, relative to the level of one of said SEQ ID NO: 1 through SEQ ID NO: 29 found in an analogous sample not having the disease or disorder, indicates the present of the disease or disorder in the subject.

122. The method of claim 121 wherein the disease or disorder is a body weight disorder.

123. The method of claim 122 wherein the body weight disorder is obesity, anorexia nervosa, bulimia nervosa, or cachexia.

124. A method of diagnosing or screening for the presence of or predisposition for developing a disease or disorder involving a body weight disorder in a subject comprising detecting one or more mutations in at least one of SEQ ID NO: 1 through SEQ ID NO: 29 in a sample derived from the subject, in which the presence of said one or more mutations indicates the presence of the disease or disorder or a predisposition for developing said disease or disorder.

125. A recombinant non-human animal that is the product of a process comprising introducing a nucleic acid encoding at least a domain of one of SEQ ID NO:

8, SEQ ID NO: [redacted], SEQ ID NO: 18, SEQ ID NO: 25, SEQ ID NO: 26, and SEQ ID NO: 27 into the non-human animal.

126. A method for confirming the association of a query QTL or a query gene in the genome of a second species with a clinical trait T exhibited by said second species, the method comprising:

(a) mapping (i) a region of the genome of a first species that comprises a first QTL or a first gene in said first species that is linked to a trait T′ to (ii) a region of the genome of said second species, wherein trait T′ is indicative of trait T; and

(b) finding a query QTL or a query gene in said second species that is potentially associated with said trait T, wherein the potential association of said query QTL or said query gene with said clinical trait T is confirmed when said query QTL or said query gene is in said region of the genome of said second species.

127. The method of claim 126, the method further comprising, prior to said mapping step (a), a step of finding said first QTL or said first gene in said first species comprising:

(i) crossing a first strain and a second strain of said first species in order to obtain a segregating population;

(ii) stratifying said segregating population into a plurality of subpopulations, wherein a subpopulation in said plurality of subpopulations represents a phenotypic extreme of said trait T′;

(iii) using cellular constituent measurements from organisms in the plurality of subpopulations to identify a cellular constituent set that exhibits a cellular constituent measurement pattern associated with said phenotypic extreme;

(iv) clustering said segregating population based on measurements of said cellular constituent set in organisms in said segregating population to obtain a plurality of population clusters; and

(v) for at least one population cluster in said plurality of population clusters, performing quantitative genetic analysis on said population cluster in order to find said first QTL or said first gene in said first species that is linked to said trait T′.

128. The method of claim 127 wherein said cellular constituent measurements are transcriptional state measurements or translational state measurements.

129. The method of claim 127 wherein said cellular constituent measurements are translational state measurements that are performed using an antibody array or two-dimensional gel electrophoresis.

130. The method of claim 127 wherein said cellular constituent set comprises a plurality of metabolites and said plurality of cellular constituent measurements are derived by a cellular phenotypic technique.

131. The method of claim 130 wherein said cellular phenotypic technique comprises a metabolomic technique wherein a plurality of levels of metabolites in one or more organisms in said segregating population is measured.

132. The method of claim 131 wherein said metabolites comprise an amino acid, a metal, a soluble sugar, or a complex carbohydrate.

133. The method of claim 127 wherein said cellular constituent measurements comprise gene expression levels, abundance of mRNA, protein expression levels, or metabolite levels.

134. The method of claim 126, the method further comprising, prior to said mapping step (a), a step of finding said first QTL or said first gene in said first species comprising:

(i) crossing a first strain and a second strain of said first species in order to obtain a segregating population;

(ii) dividing said population into a plurality of subpopulations using a classification scheme that classifies each organism in said segregating population into at least one of said subpopulations, wherein said classification scheme uses cellular constituent measurements of a plurality of cellular constituents from each said organism; and

(iii) for at least one subpopulation in said plurality of subpopulations, performing quantitative genetic analysis on said subpopulation in order to find said first QTL or said first gene in said first species that is linked to trait T'.

135. The method of claim 134 wherein said cellular constituent measurements are transcriptional state measurements or translational state measurements.

136. The method of claim 134 wherein said cellular constituent measurements are translational state measurements that are performed using an antibody array or two-dimensional gel electrophoresis.

137. The method of claim 134 wherein said plurality of cellular constituents comprise a plurality of metabolites and said plurality of cellular constituent measurements are derived by a cellular phenotypic technique.

138. The method of claim 137 wherein said cellular phenotypic technique comprises a metabolomic technique wherein a plurality of levels of metabolites in each said organism is measured.

139. The method of claim 138 wherein said metabolites comprise an amino acid, a metal, a soluble sugar, or a complex carbohydrate.

140. The method of claim 134 wherein said cellular constituent measurements of said plurality of cellular constituents comprise gene expression levels, abundance of mRNA, protein expression levels, or metabolite levels.

141. The method of claim 126, the method further comprising, prior to said mapping step (a), a step of finding said first QTL or said first gene in said first species comprising:

(i) generating a set of congenic organisms that span all or a portion of the genome of said first species using a background strain and a donor strain; and

(ii) identifying those strains in said set of congenic organisms that exhibit trait **T'**.

142. The method of claim 126 wherein said mapping step (a) is based upon a syntenic map between said first species and said second species.

143. The method of claim 126 wherein said finding step (b) comprises performing quantitative genetic analysis on a population of said second species.

144. The method of claim 126 wherein said clinical trait T is asthma, ataxia telangiectasia, bipolar disorder, cancer, common late-onset Alzheimer's disease, diabetes, heart disease, hereditary early-onset Alzheimer's disease, hereditary nonpolyposis colon cancer, hypertension, infection, maturity-onset diabetes of the young, mellitus, migraine, nonalcoholic fatty liver, nonalcoholic steatohepatitis, non-insulin-dependent diabetes mellitus, obesity, polycystic kidney disease, psoriases, schizophrenia, or xeroderma pigmentosum.

145. The method of claim 126 wherein said quantitative genetic analysis is performed using a method that uses one or more techniques selected from the group consisting of linkage analysis, a quantitative trait locus (QTL) analysis that uses a plurality of cellular constituent measurements as a phenotypic trait, and association analysis.

146. The method of claim 145 wherein said first QTL is represented by a lod score that is greater than 3.0.

147. The method of claim 145 wherein said first QTL is represented by a lod score that is greater than 4.0.

148. The method of claim 127 wherein said quantitative genetic analysis is performed using a method that uses one or more techniques selected from the group consisting of linkage analysis, a quantitative trait locus (QTL) analysis that uses a plurality of cellular constituent measurements as a phenotypic trait, and association analysis.

149. The method of claim 148 wherein said first QTL is represented by a lod score that is greater than 3.0.

150. The method of claim 148 wherein said first QTL is represented by a lod score that is greater than 4.0.

151. The method of claim 134 wherein said quantitative genetic analysis is performed using a method that uses one or more techniques selected from the group consisting of linkage analysis, a quantitative trait locus (QTL) analysis that uses a plurality of cellular constituent measurements as a phenotypic trait, and association analysis.

152. The method of claim 151 wherein said first QTL is represented by a lod score that is greater than 3.0.

153. The method of claim 151 wherein said first QTL is represented by a lod score that is greater than 4.0.

154. The method of claim 126 wherein said second species is human.

155. The method of claim 126 wherein said clinical trait **T** is obesity and said trait **T'** is high density lipoprotein level, low density lipoprotein level, very low density lipoprotein level, free fatty acid level, fat pad mass, or weight/height ratio.

156. The method of claim 126 wherein said region of the genome of said first species is a portion of a chromosome.

157. The method of claim 126 wherein said region of the genome of said first species is less than 100 centiMorgans.

158. The method of claim 126 wherein said region of the genome of said first species is less than 10 centiMorgans.

159. The method of claim 126 wherein said region of the genome of said first species is less than 5 centiMorgans.

160. The method of claim 1, the method further comprising:

(d) validating said association between said gene **G** and said clinical trait **T** by testing for genetic linkage between said expression quantitative trait loci (eQTL) and said clinical quantitative trait loci (cQTL).

161. The method of claim 160 wherein said testing for genetic linkage comprises marker-difference regression or a multiple-trait extension of composite interval mapping.

162. The computer program product of claim 58, the computer program mechanism further comprising instructions for validating said assocation between said gene **G** and said clinical trait **T** by testing for genetic linkage between said expression quantitative trait loci (eQTL) and said clinical quantitative trait loci (cQTL).

163. The computer program product of claim 162 wherein said testing for genetic linkage comprises marker-difference regression or a multiple-trait extension of composite interval mapping.

164. The computer system of claim 59, the computer the memory further comprising instructions for validating said assocation between said gene **G** and said clinical trait **T** by testing for genetic linkage between said expression quantitative trait loci (eQTL) and said clinical quantitative trait loci (cQTL).

165. The computer system of claim 164 wherein said testing for genetic linkage comprises marker-difference regression or a multiple-trait extension of composite interval mapping.

166. The method of claim 1, the method further comprising validating an association between said gene **G** and said clinical trait **T**.

167. The method of claim 166 wherein said validating comprises suppressing said gene **G** using an RNAi technique and establishing that said suppression of said gene **G** affects said eQTL.

168. A method of identifying a molecular target for a second trait in a second species, the method comprising:

(a) identifying a first gene in a segregating population that is causal for a first trait exhibited by all or a portion of said segregating population, wherein each member of said

segregating population is a member of a first species and wherein said second trait in said second species corresponds to said first trait in said first species;

(b) mapping said first gene in said first species to a corresponding locus in the genome of the second species; and

(c) determining whether a marker or a haplotype in said corresponding locus in the genome of the second species associates with said second trait, wherein, when said marker or said haplotype associates with said second trait in said second species, said locus is identified as said molecular target.

169. The method of claim 168 wherein said marker or said haplotype is in a second gene in said corresponding locus and said second gene is identified as said molecular target.

170. The method of claim 169 wherein said first gene and said second gene are orthologous.

171. The method of claim 168 wherein said identifying said first gene in said segregating population that is causal for said first trait exhibited by all or a portion of said segregating population comprises:

(a) identifying a test gene in said first species that has at least one abundance quantitative trait locus (eQTL) coincident with a respective clinical quantitative trait locus (cQTL) for said first trait; and

(b) testing, for one or more respective eQTL in said at least one eQTL, whether (i) the genetic variation of said eQTL across said segregating population and (ii) the variation of the first trait across said segregating population are correlated conditional on an abundance pattern of the test gene across said segregating population,

wherein, when the genetic variation of (1) said one or more respective eQTL tested in step (b) and (2) the variation of the first trait across said segregating population are correlated conditional on an abundance pattern of the test gene across said segregating population, said test gene is identified as said first gene.

172. The method of claim 168 wherein said second species is mammalian.

173. The method of claim 168 wherein said second species is human.

174. The method of claim 168 wherein said second trait is asthma, ataxia telangiectasia, bipolar disorder, cancer, common late-onset Alzheimer's disease, diabetes, heart disease, hereditary early-onset Alzheimer's disease, hereditary nonpolyposis colon cancer, hypertension, infection, maturity-onset diabetes of the young, mellitus, migraine, nonalcoholic fatty liver, nonalcoholic steatohepatitis, non-insulin-dependent diabetes mellitus, obesity, polycystic kidney disease, psoriases, schizophrenia, or xeroderma pigmentosum.

175. The method of claim 168 wherein said molecular target is a gene.

176. The method of claim 168 wherein said molecular target is an exon, an intron, or a regulatory element of a gene.

177. The method of claim 168 wherein said marker is a single nucleotide polymorphism, a microsatellite marker, a restriction fragment length polymorphism, a short tandem repeat, a DNA methylation marker, a sequence length polymorphism, a random amplified polymorphic DNA, an amplified fragment length polymorphisms, or a simple sequence repeat.

178. A method of identifying a molecular target for a second trait in a second species, the method comprising:

(a) identifying a first gene in a segregating population that is causal for a first trait exhibited by all or a portion of said segregating population, wherein each member of said segregating population is a member of a first species and wherein said second trait in said second species corresponds to said first trait in said first species;

(b) identifying a locus in the genome of the second species that is (1) linked to said second trait and (2) maps to the position in the genome of said first species where said first gene resides; and

(c) determining whether a marker or a haplotype in said corresponding locus in the genome of the second species associates with said second trait, wherein, when said marker or said haplotype associates with said second trait in said second species, said locus is identified as said molecular target.

179. The method of claim 178 wherein said marker or said haplotype is in a second gene in said corresponding locus and said second gene is identified as said molecular target.

180. The method of claim 179 wherein said first gene and said second gene are orthologous.

181. The method of claim 178 wherein said identifying said first gene in said segregating population that is causal for said first trait exhibited by all or a portion of said segregating population comprises:

(a) identifying a test gene in said first species that has at least one abundance quantitative trait locus (eQTL) coincident with a respective clinical quantitative trait locus (cQTL) for said first trait; and

(b) testing, for one or more respective eQTL in said at least one eQTL, whether (i) the genetic variation of said eQTL across said segregating population and (ii) the variation of the first trait across said segregating population are correlated conditional on an abundance pattern of the test gene across said segregating population,

wherein, when the genetic variation of (1) said one or more respective eQTL tested in step (a) and (2) the variation of the first trait across said segregating population are correlated conditional on an abundance pattern of the test gene across said segregating population, said test gene is identified as said first gene.

182. The method of claim 178 wherein said second species is mammalian.

183. The method of claim 178 wherein said second species is human.

184. The method of claim 178 wherein said second trait is asthma, ataxia telangiectasia, bipolar disorder, cancer, common late-onset Alzheimer's disease, diabetes, heart disease, hereditary early-onset Alzheimer's disease, hereditary nonpolyposis colon cancer, hypertension, infection, maturity-onset diabetes of the young, mellitus, migraine, nonalcoholic fatty liver, nonalcoholic steatohepatitis, non-insulin-dependent diabetes mellitus, obesity, polycystic kidney disease, psoriases, schizophrenia, or xeroderma pigmentosum.

185. The method of claim 178 wherein said molecular target is a gene.

186. The method of claim 178 wherein said molecular target is an exon, an intron, or a regulatory element of a gene.

187. The method of claim 178 wherein said marker is a single nucleotide polymorphism, a microsatellite marker, a restriction fragment length polymorphism, a short tandem repeat, a DNA methylation marker, a sequence length polymorphism, a random amplified polymorphic DNA, an amplified fragment length polymorphisms, or a simple sequence repeat.

188. A method of identifying a molecular target for a second trait in a second species, the method comprising:

(a) identifying a first gene in a segregating population that is causal for a first trait exhibited by all or a portion of said segregating population, wherein each member of said segregating population is a member of a first species and wherein said second trait in said second species corresponds to said first trait in said first species; and

(b) identifying a second gene in the genome of the second species that is orthologous to said first gene and in which (i) the variation of the abundance of the second gene across biological samples taken from a plurality of members of said second species and (ii) the variation of the second trait across said plurality of members of said second species are associated, wherein

said second gene is identified as said molecular target.

189. The method of claim 188, the method further comprising:

validating said second gene by determining whether a marker or a haplotype in said second gene associates with said second trait, wherein, when said marker or said haplotype associates with said second trait in said second species, said second gene is validated.

190. The method of claim 188 wherein said identifying said first gene in a segregating population that is causal for a first trait exhibited by all or a portion of said segregating population comprises:

(a) identifying a test gene in said first species that has at least one abundance quantitative trait locus (eQTL) coincident with a respective clinical quantitative trait locus (cQTL) for said first trait; and

(b) testing, for one or more respective eQTL in said at least one eQTL, whether (i) the genetic variation of said eQTL across said segregating population and (ii) the variation of the first trait across said segregating population are correlated conditional on an abundance pattern of the test gene across said segregating population,

wherein, when the genetic variation of (1) said one or more respective eQTL tested in step (b) and (2) the variation of the first trait across said segregating population are correlated conditional on an abundance pattern of the test gene across said segregating population, said test gene is identified as said first gene.

191. The method of claim 188 wherein said second species is mammalian.

192. The method of claim 188 wherein said second species is human.

193. The method of claim 188 wherein said second trait is asthma, ataxia telangiectasia, bipolar disorder, cancer, common late-onset Alzheimer's disease, diabetes, heart disease, hereditary early-onset Alzheimer's disease, hereditary nonpolyposis colon cancer, hypertension, infection, maturity-onset diabetes of the young, mellitus, migraine, nonalcoholic fatty liver, nonalcoholic steatohepatitis, non-insulin-dependent diabetes mellitus, obesity, polycystic kidney disease, psoriases, schizophrenia, or xeroderma pigmentosum.

194. The method of claim 188 wherein said marker is a single nucleotide polymorphism, a microsatellite marker, a restriction fragment length polymorphism, a short tandem repeat, a DNA methylation marker, a sequence length polymorphism, a random amplified polymorphic DNA, an amplified fragment length polymorphisms, or a simple sequence repeat.

195. A computer system for identifying a molecular target for a second trait in a second species, the computer system comprising:

a central processing unit;

a memory, coupled to the central processing unit, the memory storing:

instructions for identifying a first gene in a segregating population that is causal for a first trait exhibited by all or a portion of said segregating population, wherein each member of said segregating population is a member of a first species and wherein said second trait in said second species corresponds to said first trait in said first species;

instructions for mapping said first gene in said first species to a corresponding locus in the genome of the second species; and

instructions for determining whether a marker or a haplotype in said corresponding locus in the genome of the second species associates with said second trait.

196. A computer program product for use in conjunction with a computer system, the computer program product comprising a computer readable storage medium and a computer program mechanism embedded therein, the computer program mechanism comprising:

instructions for identifying a first gene in a segregating population that is causal for a first trait exhibited by all or a portion of said segregating population, wherein each member of said segregating population is a member of a first species and wherein said second trait in said second species corresponds to said first trait in said first species;

instructions for mapping said first gene in said first species to a corresponding locus in the genome of the second species; and

instructions for determining whether a marker or a haplotype in said corresponding locus in the genome of the second species associates with said second trait.

197. A computer system for identifying a molecular target for a second trait in a second species, the computer system comprising:

a central processing unit;

a memory, coupled to the central processing unit, the memory storing:

instructions for identifying a first gene in a segregating population that is causal for a first trait exhibited by all or a portion of said segregating population, wherein each member of said segregating population is a member of a first species and wherein said second trait in said second species corresponds to said first trait in said first species;

instructions for identifying a locus in the genome of the second species that is (1) linked to said second trait and (2) maps to the position in the genome of said first species where said first gene resides; and

instructions for determining whether a marker or a haplotype in said corresponding locus in the genome of the second species associates with said second trait.

198. A computer program product for use in conjunction with a computer system, the computer program product comprising a computer readable storage medium and a computer program mechanism embedded therein, the computer program mechanism comprising:

instructions for identifying a first gene in a segregating population that is causal for a first trait exhibited by all or a portion of said segregating population, wherein each member of said segregating population is a member of a first species and wherein said second trait in said second species corresponds to said first trait in said first species;

instructions for identifying a locus in the genome of the second species that is (1) linked to said second trait and (2) maps to the position in the genome of said first species where said first gene resides; and

instructions for determining whether a marker or a haplotype in said corresponding locus in the genome of the second species associates with said second trait.

199. A computer system for identifying a molecular target for a second trait in a second species, the computer system comprising:

a central processing unit;

a memory, coupled to the central processing unit, the memory storing:

instructions for identifying a first gene in a segregating population that is causal for a first trait exhibited by all or a portion of said segregating population, wherein each member of said segregating population is a member of a first species and wherein said second trait in said second species corresponds to said first trait in said first species; and

instructions for identifying a second gene in the genome of the second species that is orthologous to said first gene and in which (i) the variation of the abundance of the second gene across biological samples taken from a plurality of members of said second species and (ii) the variation of the second trait across said plurality of members of said second species are associated.

200. A computer program product for use in conjunction with a computer system, the computer program product comprising a computer readable storage medium

and a computer program mechanism embedded therein, the computer program mechanism comprising:

instructions for identifying a first gene in a segregating population that is causal for a first trait exhibited by all or a portion of said segregating population, wherein each member of said segregating population is a member of a first species and wherein said second trait in said second species corresponds to said first trait in said first species; and

instructions for identifying a second gene in the genome of the second species that is orthologous to said first gene and in which (i) the variation of the abundance of the second gene across biological samples taken from a plurality of members of said second species and (ii) the variation of the second trait across said plurality of members of said second species are associated.